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Letter to the Editor

Gene Localisation for Wilson-Turner Syndrome (WTS:MIM 309585)

To the Editor:

The gene for this syndrome of X-linked mental retardation with gynaecomastia, obesity, speech difficulties, tapering fingers and small feet was mapped between Xp21.1 and Xq22 [Wilson et al., 1991]. Linkage to *DXS255* at Xp11 was firmly established, with no recombination. Subsequent characterisation of numerous microsatellite markers and development of the background genetic map in this region of the X chromosome has enabled significant reduction to the localisation of the gene for WTS in the one family so far reported.

The new linkage data were obtained as described previously [Gedeon et al., 1994] and are presented in Table I. The closest flanking markers are *DXS426* at Xp11.3 and *DXS990* at Xq21.3. The regional localisation is significantly reduced from the previous interval of 66 cM to an interval of 25 cM. The maximum two-point lod score is now 6.07 at *AR*.

Similar syndromes must be considered in the differential diagnosis of WTS. Both the specific clinical findings and gene localisations distinguish WTS from Börjeson-Forssman-Lehman syndrome [Wilson et al., 1991; Gedeon et al., 1996] although gynaecomastia and obesity occur in both syndromes. Frézal [1992] saw the resemblance between WTS and the unmapped syndrome reported by Fasquez et al. [1979], but Turner [1992] suggested that the Vasquez et al. [1979] patients had Börjeson-Forssman-Lehmann syndrome. Mapping the gene in the Vasquez et al. family would resolve these alternatives. Gene localisation in the first in-

TABLE I. Two-Point Lod Scores Between WTS and 22 Marker Loci

	θ								
Loci	0.001	0.01	0.05	0.1	0.2	0.3	0.4	Zmax	θmax
DXS538	−6.21	−2.27	0.22	1.04	1.42	1.21	0.72	1.42	0.20
DXS7	2.94	3.86	4.20	4.03	3.31	2.35	1.22	4.20	0.05
MAOA	0.93	1.87	2.29	2.23	1.78	1.18	0.55	2.30	0.06
DXS1003	2.53	3.46	3.81	3.66	2.98	2.07	1.00	3.81	0.05
SYN1	2.12	3.05	3.42	3.31	2.72	1.94	1.01	3.42	0.06
PFC	1.03	1.98	2.42	2.40	2.01	1.44	0.75	2.44	0.07
DXS426	0.59	1.54	1.98	1.97	1.62	1.13	0.58	2.00	0.07
DXS573	3.13	3.08	2.87	2.59	2.01	1.39	0.73	3.13	0.00
DXS255	5.76	5.67	5.29	4.78	3.71	2.53	1.26	5.76	0.00
DXS991	4.65	4.58	4.27	3.86	3.00	2.07	1.06	4.65	0.00
AR	6.06	5.97	5.59	5.08	4.00	2.79	1.45	6.06	0.00
DXS1125	5.11	5.04	4.71	4.28	3.35	2.32	1.19	5.11	0.00
DXS106	3.43	3.38	3.15	2.84	2.21	1.54	0.81	3.43	0.00
DXS453	5.64	5.56	5.20	4.73	3.71	2.57	1.31	5.65	0.00
DXS559	2.78	2.74	2.54	2.28	1.72	1.11	0.47	2.78	0.00
DXS566	5.41	5.33	4.99	4.53	3.56	2.47	1.27	5.41	0.00
DXS227	5.84	5.75	5.37	4.87	3.79	2.59	1.26	5.84	0.00
DXS986	2.95	2.90	2.67	2.38	1.77	1.13	0.50	2.95	0.00
DXS3	4.53	4.46	4.15	3.76	2.92	2.02	1.04	4.53	0.00
DXS990	1.65	2.58	2.98	2.90	2.39	1.69	0.88	2.98	0.06
DXS178	−7.11	−3.16	−0.59	0.32	0.89	0.88	0.57	0.93	0.25
DXS571	−4.05	−1.11	0.70	1.24	1.39	1.11	0.62	1.41	0.17

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stance, then mutation identification where regional localisations overlap, provides definitive resolution of the alternatives of genetic heterogeneity or genetic homogeneity for disorders with similar manifestations. The refined regional localisation now presented for WTS should be useful at least to exclude allelism for any X-linked disorders with features of WTS but with gene localisations distinct from WTS.

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